

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of: Loughney

Serial No. To be assigned

Filed: Herewith

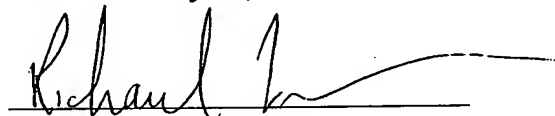
For: Phosphodiesterase 10

Group Art Unit: To be assigned

Examiner: To be assigned

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) Date: February 26, 2002
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 Richard Zimmermann

TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING

Assistant Commissioner for Patents
 Washington, DC 20231

Sir:

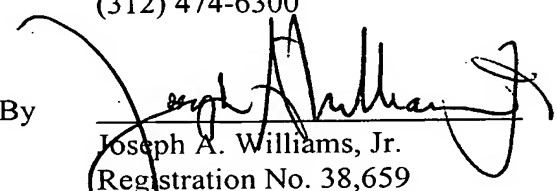
The Applicants respectfully request entry of the substitute Sequence Listing filed herewith. The substitute Sequence Listing corrects errors that were identified during the prosecution of the parent application (USSN 09/256,000) and is included at this time to expedite prosecution.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same, and that the substitute Sequence Listing includes no new matter.

Respectfully submitted,

MARSHALL, GERSTEIN & BORUN
 6300 Sears Tower
 233 South Wacker Drive
 Chicago, Illinois 60606-6357
 (312) 474-6300

By


 Joseph A. Williams, Jr.
 Registration No. 38,659
 Attorney for Applicants

February 26, 2002

20020226 0256300

SEQUENCE LISTING

<110> Loughney, Kate
 <120> Phosphodiesterase 10
 <130> 27866/35308
 <140> 09/256,000
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 <150> 60/075,508
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 10 15 20 25
 atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
 30 35 40
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 45 50 55
 gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
 60 65 70
 tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
 75 80 85
 agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
 90 95 100 105
 aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388

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Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His		
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Asn	Phe	Arg	His	Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val		
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Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
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Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn		
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gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	gcc	ttc	cag	atc	820	
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile		
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ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	cca	cct	gat	ggg	868	
Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly		
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ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	ttg	gcc	act	gac	916	
Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp		
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ttg	ata	aaa	tgc	tgt	gat	atc	tct	aac	gag	gtc	cgt	cca	atg	gaa	gtc	1060	
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Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser	350	355	360	
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga				1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg	365	370	375	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc				1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val	380	385	390	
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag				1252
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu	395	400	405	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag				1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu	410	415	420	425
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac				1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp	430	435	440	
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat				1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp	445	450	455	
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg				1443
Val Lys Asn Ser Glu Gly Asp Cys Ala	460	465		
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Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala	35	40	45	
Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu	50	55	60	

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Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	115	120	125	
Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	130	135	140	
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Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	165	170	175	
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Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	195	200	205	
Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	210	215	220	
His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	225	230	235	240
Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	245	250	255	
His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	260	265	270	
Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	275	280	285	
Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	290	295	300	
Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	305	310	315	320
Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	325	330	335	
Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	340	345	350	
Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly	355	360	365	

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
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Cys Ala
465

<210> 3

<211> 225

<212> DNA

<213> Homo sapiens

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<223> Nucleotides at positions 130, 186, and 205 are
either A, T, G, or C.

<400> 3

agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60
accaaggcca cagcccagat tgggttcac aagtttgccc tgatcccaat gtttgaaaca 120
gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccg 180
gatcgntacg aggagctgaa gcggn tagat gacgcatga aagag 225

<210> 4

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 12, 36, 61, and 109 are
either A, T, G, or C.

<400> 4

gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60
gnaaccacca ctgcgcggtg gccttcgaga tctcgcgga gcctgagtgn aacatcttct 120
ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 14, 22, and 50 are either
A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gncttccaga tctctgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411
are either A, T, G, or C.

<400> 6
nggttaactg ggcacatctg tctttctctg agaacagcga tctggttatg gggcatttct 60
gtctctaattg tcaactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccgtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tccaatggtt tgaaacagtg accaagctct tccccatggg 240
ttgagggaga ttcattgctgg cagccanttt ggggaatccc gaggattcgc tacgagggag 300
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagttttga agttttgggg gggccaccga ggaagtccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,
and 396 are either A, T, G, or C.

<400> 7
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ggagctcttc cctgcacaag gntcccgcgc antcggccag cccgtccaga actgcagcca 120
cgccccccgn tttcctcagg cacagtctcc ttactgttt ttacatctc tgcttctctc 180
tctggacttc toggtgggcc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

gggcgtcatc tatccgcttc agtcctcgt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat ctctctcaac catggggggg aggagcttgg ggactngtt ttcaaaaatt 360
gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cttttggggc 420
aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203, 206, 238, 252, 297, 370, 389, and 427 are either A, T, G, or C.

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gtncagggtg cccagggagc tcttccctgc acaaggancc cgcgcantcg gccagcccgt 120
ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180
atctctgntt ctctctctgg gantntcgg tgggccccag aacgtcaagc tgtcagtntt 240
cttctgtaac tntttcatgg gcgtcatcta tccgtttcag ctctctcgta ggcatnttg 300
gggattccca aagtgggctg gcagcatgga tcttctcaa accatggggg gaaggagttt 360
gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaaccaatt 420
atgggggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
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tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tcctgatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA

<213> Mus musculus

<400> 10

gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcac caagtttgtc 240
tgtccaatgt 250

<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

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<223> Nucleotides at positions 155, 393, and 442 are
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aatggagaat ttgactaca gcaacgagga gcacatgacc ctggtgagt gcttattctg 120
cctgggtggg cagccaggcg gttgggctgg cgaanagggt catccatcca gctcacactg 180
gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240
caaggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggcctcct 300
tcatggtcag aggcagcatt ctccattcc tccatctctt ttgggatttt gaaggagata 360
aagtgggggtg aaggccgtgc attctcgctc tgnntttcca gagaattaa accagttttc 420
ccttgaaggc acagccccag cntggcattt tgaaagtgt 459

<210> 12

<211> 599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99) .. (443)

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agaacagcga tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116
Cys His Cys Leu Leu His
1 5

tcc	ctg	cag	agc	gac	cgt	gag	aag	tca	gaa	ggc	ctt	ccc	gtg	gcc	ccg	164
Ser	Leu	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	
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ttc	atg	gac	cga	gac	aaa	gtg	acc	aag	gcc	aca	gcc	cag	att	ggg	ttc	212
Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	
		25					30					35				
atc	aag	ttt	gtc	ctg	atc	cca	atg	ttt	gaa	aca	gtg	acc	aag	ctc	ttc	260
Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	
	40					45					50					
ccc	atg	gtt	gag	gag	atc	atg	ctg	cag	cca	ctt	tgg	gaa	tcc	cga	gat	308
Pro	Met	Val	Glu	Glu	Ile	Met	Leu	Gln	Pro	Leu	Trp	Glu	Ser	Arg	Asp	
	55				60				65						70	
cgc	tac	gag	gag	ctg	aag	cgg	ata	gat	gac	gcc	atg	aaa	gag	tta	cag	356
Arg	Tyr	Glu	Glu	Leu	Lys	Arg	Ile	Asp	Asp	Ala	Met	Lys	Glu	Leu	Gln	
				75					80					85		
aag	aag	act	gac	agc	ttg	acg	tct	ggg	gcc	acc	gag	aag	tcc	aga	gag	404
Lys	Lys	Thr	Asp	Ser	Leu	Thr	Ser	Gly	Ala	Thr	Glu	Lys	Ser	Arg	Glu	
			90					95					100			
aga	agc	aga	gat	gtg	aaa	aac	agt	gaa	gga	gac	tgt	gcc	tgagg	aaa	agc	453
Arg	Ser	Arg	Asp	Val	Lys	Asn	Ser	Glu	Gly	Asp	Cys	Ala				
		105				110					115					
ggggggc	gtg	gctgcag	ttc	tggac	ggg	ct	ggccgag	ctg	cg	gggat	cc	ttgtgcag	gg			513
aagag	ctgcc	ctgggcac	ct	ggcacc	acaa	gaccat	gttt	tctaaga	acc	attttgt	tca					573
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<210> 13
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 <212> PRT
 <213> Homo sapiens

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 Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala
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 35 40 45
 Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50 55 60
 Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65 70 75 80
 Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala

85

90

95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
 100 105 110

Asp Cys Ala
 115

<210> 14
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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<210> 15
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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 <213> Homo sapiens

<220>
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 <222> (107)..(1066)

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cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115
 Ala Leu Glu
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cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
 His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
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gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
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Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val	Ala	Gln	Met	Met	
				40					45					50		
tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	ttc	tca	caa	acg	307
Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	
			55					60					65			
gat	atc	ctg	atc	cta	atg	aca	gcg	gcc	atc	tgc	cac	gat	ctg	gac	cat	355
Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His	Asp	Leu	Asp	His	
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Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	
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gtc	cgc	tac	aat	gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	451
Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	
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gcc	ttc	cag	atc	ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	499
Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	
				120					125					130		
cca	cct	gat	ggg	ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	547
Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	
			135					140					145			
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Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	
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gag	aaa	atg	gag	aat	ttt	gac	tac	agc	aac	gag	gag	cac	atg	acc	ctg	643
Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	Met	Thr	Leu	
	165					170					175					
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Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	
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Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	
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Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	
			215					220					225			
ttc	atg	gac	cga	gac	aaa	gtg	acc	aag	gcc	aca	gcc	cag	att	ggg	ttc	835
Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	
			230				235					240				
atc	aag	ttt	gtc	ctg	atc	cca	atg	ttt	gaa	aca	gtg	acc	aag	ctc	ttc	883
Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	
	245					250					255					
ccc	atg	gtt	gag	gag	atc	atg	ctg	cag	cca	ctt	tgg	gaa	tcc	cga	gat	931

Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
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Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
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Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
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Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
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Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
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Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
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Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
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Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
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Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
130 135 140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
165 170 175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
210 215 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
225 230 235 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
245 250 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
260 265 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
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Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala
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atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
15 20 25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
30 35 40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg	253
Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Asp Asp Ala Met	
45 50 55 60	
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Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr	
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Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu	
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Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
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aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
110 115 120	
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	
125 130 135 140	
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Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	
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Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
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Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	
175 180 185	
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Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	
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Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	
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Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	
225 230 235	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac	829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	
240 245 250	
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Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	
255 260 265	
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc	925

Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
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cta	atg	aca	gcg	gcc	atc	tgc	cac	gat	ctg	gac	cat	ccc	ggc	tac	aac	973	
Leu	Met	Thr	Ala	Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn		
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aac	acg	tac	cag	atc	aat	gcc	cgc	aca	gag	ctg	gcg	gtc	cgc	tac	aac	1021	
Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn		
				305					310					315			
gac	atc	tca	ccg	ctg	gag	aac	cac	cac	tgc	gcc	gtg	gcc	ctc	cag	atc	1069	
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile		
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ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	cca	cct	gat	ggg	1117	
Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly		
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ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	ttg	gcc	act	gac	1165	
Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp		
	350					355					360						
atg	gca	aga	cat	gca	gaa	att	atg	gat	tct	ttc	aaa	gag	aaa	atg	gag	1213	
Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu		
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Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile		
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ttg	ata	aaa	tgc	tgt	gat	atc	tct	aac	gag	gtc	cgt	cca	atg	gaa	gtc	1309	
Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val		
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gca	gag	cct	tgg	gtg	gac	tgt	tta	tta	gag	gaa	tat	ttt	atg	cag	agc	1357	
Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser		
		415					420					425					
gac	cgt	gag	aag	tca	gaa	ggc	ctt	cct	gtg	gca	ccg	ttc	atg	gac	cga	1405	
Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg		
	430					435					440						
gac	aaa	gtg	acc	aag	gcc	aca	gcc	cag	att	ggg	ttc	atc	aag	ttt	gtc	1453	
Asp	Lys	Val	Thr	Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val		
445					450					455					460		
ctg	atc	cca	atg	ttt	gaa	aca	gtg	acc	aag	ctc	ttc	ccc	atg	gtt	gag	1501	
Leu	Ile	Pro	Met	Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu		
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gag	atc	atg	ctg	cag	cca	ctt	tgg	gaa	tcc	cga	gat	cgc	tac	gag	gag	1549	
Glu	Ile	Met	Leu	Gln	Pro	Leu	Trp	Glu	Ser	Arg	Asp	Arg	Tyr	Glu	Glu		
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ctg	aag	cgg	ata	gat	gac	gcc	atg	aaa	gag	tta	cag	aag	aag	act	gac	1597	
Leu	Lys	Arg	Ile	Asp	Asp	Ala	Met	Lys	Glu	Leu	Gln	Lys	Lys	Thr	Asp		

495 500 505
 agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 1645
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 gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggctg 1692
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 525 530
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 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
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 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
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 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
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 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
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 Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140
 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
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 Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
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Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	180	185	190
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	195	200	205
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	210	215	220
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	225	230	235
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	245	250	255
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	260	265	270
Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	275	280	285
Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	290	295	300
Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	305	310	315
Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	325	330	335
Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	340	345	350
Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	355	360	365
Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	370	375	380
Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	385	390	395
Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	405	410	415
Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	420	425	430
Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	435	440	445
Lys	Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	450	455	460
Phe	Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu	Glu	Ile	Met	Leu	465	470	475

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
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Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
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Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
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aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
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cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu

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aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu 165 170 175			529
ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile 180 185 190			577
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ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220			673
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240			721
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255			769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270			817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285			865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300			913
ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305 310 315 320			961
cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335			1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340 345 350			1057
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365			1105

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag 1153
 Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380

tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga 1201
 Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400

cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca 1249
 Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415

gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc 1297
 Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430

aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt 1345
 Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445

gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg 1393
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460

gag tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca 1441
 Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480

gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag 1489
 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495

gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt 1537
 Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510

gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag 1585
 Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525

cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat 1633
 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540

gag gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg 1681
 Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
 545 550 555 560

gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa 1729
 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
 565 570 575

gga gac tgt gcc tgaggaaagc ggggggcgtg gctgcagttc tggacgggct 1781
 Gly Asp Cys Ala
 580

ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841

gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaaa ggaattcatg 1901
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 Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
 35 40 45
 Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
 50 55 60
 Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65 70 75 80
 Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
 85 90 95
 Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
 100 105 110
 Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
 115 120 125
 Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
 130 135 140
 Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
 145 150 155 160
 Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
 165 170 175
 Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
 180 185 190
 Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
 195 200 205
 Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
 210 215 220
 Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
 225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
245 250 255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
260 265 270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
275 280 285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
435 440 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
450 455 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
530 535 540

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ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggagc agg atg gga tcc ggc 175
Met Gly Ser Gly
1

tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
5 10 15 20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
25 30 35

gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
40 45 50

ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
55 60 65

gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
70 75 80

caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
85 90 95 100

gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
105 110 115

gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga 559

Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly		
			120					125					130				
cta	aaa	gtg	gtg	gag	att	gag	aaa	tgc	aag	agt	gac	att	aag	aag	atg	607	
Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met		
		135					140					145					
agg	gag	gag	ctg	gcg	gcc	aga	agc	agc	agg	acc	aac	tgc	ccc	tgt	aag	655	
Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys		
		150				155					160						
tac	agt	ttt	ttg	gat	aac	cac	aag	aag	ttg	act	cct	cga	cgc	gat	gtt	703	
Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val		
					170					175					180		
ccc	act	tac	ccc	aag	tac	ctg	ctc	tct	cca	gag	acc	atc	gag	gcc	ctg	751	
Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu		
				185					190					195			
cgg	aag	ccg	acc	ttt	gac	gtc	tgg	ctt	tgg	gag	ccc	aat	gag	atg	ctg	799	
Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu		
			200					205					210				
agc	tgc	ctg	gag	cac	atg	tac	cac	gac	ctc	ggg	ctg	gtc	agg	gac	ttc	847	
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe		
			215				220					225					
agc	atc	aac	cct	gtc	acc	ctc	agg	agg	tgg	ctg	ttc	tgc	gtc	cac	gac	895	
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp		
			230			235					240						
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	cgg	cac	tgc	ttc	tgc	gtg	943	
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val		
					250				255						260		
gcc	cag	atg	atg	tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	991	
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys		
				265				270						275			
ttc	tca	caa	acg	gat	atc	ctg	atc	cta	atg	aca	gcg	gcc	atc	tgc	cac	1039	
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His		
			280					285					290				
gat	ctg	gac	cat	ccc	ggc	tac	aac	aac	acg	tac	cag	atc	aat	gcc	cgc	1087	
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg		
			295				300					305					
aca	gag	ctg	gcg	gtc	cgc	tac	aat	gac	atc	tca	ccg	ctg	gag	aac	cac	1135	
Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His		
			310			315					320						
cac	tgc	gcc	gtg	gcc	ttc	cag	atc	ctc	gcc	gag	cct	gag	tgc	aac	atc	1183	
His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile		
					330				335						340		
ttc	tcc	aac	atc	cca	cct	gat	ggg	ttc	aag	cag	atc	cga	cag	gga	atg	1231	
Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met		

	345	350	355	
atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg				1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met				
	360	365	370	
gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag				1327
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu				
	375	380	385	
cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct				1375
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser				
	390	395	400	
aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta				1423
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu				
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tta gag gaa tat ttt atg cag agc gac cgt gaga				1457
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg				
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 35 40 45
 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60
 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80
 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95
 Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110
 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125
 Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140
 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn

145		150		155		160									
Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro
				165					170					175	
Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr
			180					185					190		
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro
		195				200						205			
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu
	210					215					220				
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe
225					230					235					240
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His
				245					250					255	
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser
			260					265					270		
Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala
		275					280						285		
Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln
	290					295					300				
Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro
305					310					315					320
Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro
				325					330					335	
Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile
			340					345					350		
Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His
		355					360					365			
Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr
	370					375					380				
Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys
385					390					395					400
Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp
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<210> 25

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 26

cgaggagtca acttcttg 18

SEQUENCE LISTING



<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

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<170> PatentIn Ver. 2.0

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Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu	
10 15 20 25	
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc	148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe	
30 35 40	
aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta	196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu	
45 50 55	
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa	244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys	
60 65 70	
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc	292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser	
75 80 85	
agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag	340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys	
90 95 100 105	
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc	388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu	
110 115 120	
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg	436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp	
125 130 135	
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac	484
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His	
140 145 150	
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg	532
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	
155 160 165	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac	580
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	
170 175 180 185	
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc	628
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	
190 195 200	

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gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile 250 255 260 265	820
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly 270 275 280	868
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp 285 290 295	916
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gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser 350 355 360	1108
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg 365 370 375	1156
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ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
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 395 400 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
 410 415 420 425

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
 430 435 440

agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
 445 450 455

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1443
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 460 465

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503

ctggggcacct ggcaccacaa gaccatgttt tctaagaacc atttt 1548

<210> 2

<211> 466

<212> PRT

<213> Homo sapiens

<400> 2

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Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
 20 25 30

Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
 35 40 45

Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
 50 55 60

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
65 70 75 80

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
450 455 460

Cys Ala

465

<210> 3

<211> 225

<212> DNA

<213> Homo sapiens

<400> 3

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gtgaccaagn tcttccccat gggtgaggag atcatgctgc agccactttg ggaatcccga 180
gatcgnatcg aggagctgaa gcggnatgat gacgccatga aagag 225

<210> 4

<211> 158

<212> DNA

<213> Homo sapiens

<400> 4

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gnaaccacca ctgcgccgtg gccttcaga tcctcgccga gcctgagtgn aacatcttct 120
ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5

<211> 98

<212> DNA

<213> Homo sapiens

<400> 5

gagaacacca ctgngccgtg gnettcaga tcctcgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6

<211> 418

<212> DNA

<213> Homo sapiens

<400> 6

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gtctctaatag tcaactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccggtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatggt tgaacacagt accaagctct tccccatggg 240
ttgagggaga ttcattgctg cagccanttt ggggaatccc gaggattcgc tacgagggag 300
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagttttga agttttgggg gggccaccga ggaagtccn ggaggaggag naggcaga 418

<210> 7

<211> 428

<212> DNA

<213> Homo sapiens

<400> 7

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ggagctcttc cctgcacaag gntcccgcgc antcggccag cccgtccaga actgcagcca 120
cgccccccgn tttcttcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180
tctggacttc tcgggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240
gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat ctctctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360

gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

aatttttg

428

<210> 8

<211> 438

<212> DNA

<213> Homo sapiens

<400> 8

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gtncacagtg cccagggagc tcttccttgc acaaggancc cgcgcantcg gccagcccgt 120

ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180

atctctgntt ctctctctgg gantnttcgg tgggccccag aacgtcaagc tgtcagtntt 240

cttctgtaac tntttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300

gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360

gggtcaattn ttttcaaaac attgggggnt cagggacaaa attttgatgg aaaccaatt 420

tgggggntgt gggccttg

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<210> 9

<211> 262

<212> DNA

<213> Mus musculus

<400> 9

gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat ttcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tcctgatccc aatgtttgaa ac 262

<210> 10

<211> 250

<212> DNA

<213> Mus musculus

<400> 10

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tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgc 240
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<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

<400> 11

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cctgggtggg cagccaggcg gttgggctgg cgaanagggt catccatcca gctcacactg 180
gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240
caaggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggctctcct 300
tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360
aagtggggtg aaggccgtgc attctcgtc tgnttttcca gagaattaaa accagttttc 420
ccttgaaggc acagccccag cntggcattt tgaaagttg 459

<210> 12

<211> 599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99) .. (443)

<400> 12

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agaacagcga tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116
Cys.His Cys Leu Leu His
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
10 15 20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
25 30 35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 260
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
40 45 50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 308
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
55 60 65 70

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 356
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
75 80 85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 404
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
90 95 100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
105 110 115

ggggggcggtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 513

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 573

ctgatacaaa aaaaaaaaaa aaaaaa 599

<210> 13

<211> 115

<212> PRT

<213> Homo sapiens

<400> 13

Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
1 5 10 15

-13-

Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala
20 25 30

Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
85 90 95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
100 105 110

Asp Cys Ala
115

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

agtcgaattc accgtgagaa gtcagaag

28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gtcaaagctt acatggtctt gtggtgcc

28

<210> 16

<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)..(1066)

<400> 16

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Ala Leu Glu
1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
70 75 80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg 403
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
85 90 95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg	451
Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val	
100 105 110 115	
gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc	499
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile	
120 125 130	
cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc	547
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile	
135 140 145	
ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa	595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys	
150 155 160	
gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg	643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu	
165 170 175	
ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt	691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg	
180 185 190 195	
cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat	739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr	
200 205 210	
ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg	787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro	
215 220 225	
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc	835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe	
230 235 240	
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc	883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe	
245 250 255	
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat	931
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp	
260 265 270 275	
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag	979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln	
280 285 290	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag	1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu	
295 300 305	

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aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc    1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
          310                      315                      320

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ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 1136

aagagctgcc ctgggcacct. ggcaccacaa gaccatgttt tctaagaacc attttgttca 1196

ctgatacaaa aaaaaaaaaag gaattcatga tgctgtacag aattttattt ttaaactgtc 1256

ttttaaataa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaa 1303

<210> 17

<211> 320

<212> PRT

<213> Homo sapiens

<400> 17

Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser
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Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn
20 25 30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
35 40 45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
50 55 60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
65 70 75 80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
85 90 95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
100 105 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
130 135 140

Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	
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Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	
				165					170					175		
Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	
			180					185					190			
Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu	Leu	
		195					200					205				
Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	
	210					215					220					
Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	Ala	Thr	Ala	Gln	
225					230					235					240	
Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	Glu	Thr	Val	Thr	
				245					250					255		
Lys	Leu	Phe	Pro	Met	Val	Glu	Glu	Ile	Met	Leu	Gln	Pro	Leu	Trp	Glu	
			260					265					270			
Ser	Arg	Asp	Arg	Tyr	Glu	Glu	Leu	Lys	Arg	Ile	Asp	Asp	Ala	Met	Lys	
		275					280					285				
Glu	Leu	Gln	Lys	Lys	Thr	Asp	Ser	Leu	Thr	Ser	Gly	Ala	Thr	Glu	Lys	
	290					295					300					
Ser	Arg	Glu	Arg	Ser	Arg	Asp	Val	Lys	Asn	Ser	Glu	Gly	Asp	Cys	Ala	
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<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(1672)

<400> 18

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	Met	Gly	Ser	Gly	Ser	Ser	Ser	Tyr	Arg	Pro	Lys	Ala				
	1				5					10						
atc	tac	ctg	gac	atc	gat	gga	cgc	att	cag	aag	gta	atc	ttc	agc	aag	157
Ile	Tyr	Leu	Asp	Ile	Asp	Gly	Arg	Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	
		15				20						25				
tac	tgc	aac	tcc	agc	gac	atc	atg	gac	ctg	ttc	tgc	atc	gcc	acc	ggc	205
Tyr	Cys	Asn	Ser	Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	
	30					35					40					
ctg	cct	cgg	aac	acg	acc	atc	tcc	ctg	ctg	acc	acc	gac	gac	gcc	atg	253
Leu	Pro	Arg	Asn	Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	
	45					50				55					60	
gtc	tcc	atc	gac	ccc	acc	atg	ccc	gcg	aat	tca	gaa	cgc	act	ccg	tac	301
Val	Ser	Ile	Asp	Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	
				65					70					75		
aaa	gtg	aga	cct	gtg	gcc	atc	aag	caa	ctc	tcc	gag	aga	gaa	gaa	tta	349
Lys	Val	Arg	Pro	Val	Ala	Ile	Lys	Gln	Leu	Ser	Glu	Arg	Glu	Glu	Leu	
			80					85					90			
atc	cag	agc	gtg	ctg	gcg	cag	gtt	gca	gag	cag	ttc	tca	aga	gca	ttc	397
Ile	Gln	Ser	Val	Leu	Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	
		95					100					105				
aaa	atc	aat	gaa	ctg	aaa	gct	gaa	gtt	gca	aat	cac	ttg	gct	gtc	cta	445
Lys	Ile	Asn	Glu	Leu	Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	
	110					115					120					
gag	aaa	cgc	gtg	gaa	ttg	gaa	gga	cta	aaa	gtg	gtg	gag	att	gag	aaa	493
Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	
	125				130					135				140		
tgc	aag	agt	gac	att	aag	aag	atg	agg	gag	gag	ctg	gcg	gcc	aga	agc	541
Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	
			145					150						155		
agc	agg	acc	aac	tgc	ccc	tgt	aag	tac	agt	ttt	ttg	gat	aac	cac	aag	589
Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	
			160					165					170			
aag	ttg	act	cct	cga	cgc	gat	gtt	ccc	act	tac	ccc	aag	tac	ctg	ctc	637
Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	
		175					180					185				
tct	cca	gag	acc	atc	gag	gcc	ctg	cgg	aag	ccg	acc	ttt	gac	gtc	tgg	685
Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	
	190					195					200					
ctt	tgg	gag	ccc	aat	gag	atg	ctg	agc	tgc	ctg	gag	cac	atg	tac	cac	733
Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	
205					210				215					220		

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg	781
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg	
225 230 235	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac	829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His	
240 245 250	
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc	877
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val	
255 260 265	
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc	925
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile	
270 275 280	
cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac	973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn	
285 290 295 300	
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Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn	
305 310 315	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc	1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile	
320 325 330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg	1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly	
335 340 345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac	1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp	
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Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu	
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Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile	
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Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val	
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Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser	
415 420 425	
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Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg	
430 435 440	

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc 1453
 Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
 445 450 455 460

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1501
 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
 465 470 475

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1549
 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
 480 485 490

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1597
 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
 495 500 505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 1645
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
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 Val Lys Asn Ser Glu Gly Asp Cys Ala
 525 530

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1752

ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca ctgataaaaa 1812

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<212> PRT

<213> Homo sapiens

<400> 19

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 35 40 45

Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val	Ser	Ile	Asp	50	55	60	
Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys	Val	Arg	Pro	65	70	75	80
Val	Ala	Ile	Lys	Gln	Leu	Ser	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val	85	90	95	
Leu	Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu	100	105	110	
Leu	Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	115	120	125	
Glu	Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	130	135	140	
Ile	Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	145	150	155	160
Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	165	170	175	
Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	180	185	190	
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	195	200	205	
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	210	215	220	
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	225	230	235	240
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	245	250	255	
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	260	265	270	

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
420 425 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
485 490 495

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<210> 20

<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2) .. (1741)

<400> 20

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  Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
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  Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
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  Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
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aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
  Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
    85             90             95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
  Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
   100             105             110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
  Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
   115             120             125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
  Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
   130             135             140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
  Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
  145             150             155             160

aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa 529
  Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
   165             170             175

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180 185 190	
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Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys	
195 200 205	
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga	673
Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg	
210 215 220	
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc	721
Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile	
225 230 235 240	
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat	769
Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn	
245 250 255	
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc	817
Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val	
260 265 270	
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Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys	
275 280 285	
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Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys	
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Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu	
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Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala	
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Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile	
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Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu	
370 375 380	
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Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg	
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Gln Gly Met Il Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala	
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gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc	1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser	
420 425 430	
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Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys	
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Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val	
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Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser	
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Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys	
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530 535 540	
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Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly	
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Gly Asp Cys Ala	
580	
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<210> 21

<211> 580

<212> PRT

<213> Homo sapiens

<400> 21

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Pro	Arg	Asn	Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val
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Ser	Ile	Asp	Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys
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Val	Arg	Pro	Val	Ala	Ile	Lys	Gln	Leu	Ser	Ala	Asp	Val	Glu	Asp	Lys
65					70					75					80
Arg	Thr	Thr	Ser	Arg	Gly	Gln	Ser	Ala	Glu	Arg	Pro	Leu	Arg	Asp	Arg
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Gly	Gln	Val	Glu	Pro	Arg	Pro	Arg	Glu	Pro	Gln	Gly	Cys	Tyr	Gln	Glu
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Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys
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Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	
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Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	
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Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	
			340					345					350			
Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	
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Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	
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Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	
			405						410					415		
Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	
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Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	
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Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	
	450					455					460					
Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	
465					470					475					480	
Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	
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Ala	Thr	Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	
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Glu	Thr	Val	Thr	Lys	Leu	Phe	Pro	Met	Val	Glu	Glu	Ile	Met	Leu	Gln	
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Pro	Leu	Trp	Glu	Ser	Arg	Asp	Arg	Tyr	Glu	Glu	Leu	Lys	Arg	Ile	Asp	
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<210> 22

<211> 1457

<212> DNA

<213> Homo sapiens

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Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
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gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
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Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly	
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Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met	
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agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag	655
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys	
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Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val	
165 170 175 180	
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Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu	
185 190 195	
cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg	799
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu	
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Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe	
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Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp	
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aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg	943
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val	
245 250 255 260	
gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc cag gag aag	991
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys	
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Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His	
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Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg	
295 300 305	
aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac	1135
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His	
310 315 320	

cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag tgc aac atc 1183
 His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
 325 330 335 340

 ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg 1231
 Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
 345 350 355

 atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg 1279
 Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
 360 365 370

 gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag 1327
 Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
 375 380 385

 cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct 1375
 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
 390 395 400

 aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta 1423
 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
 405 410 415 420

 tta gag gaa tat ttt atg cag agc gac cgt gaga 1457
 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
 425 430

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<211> 430

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
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 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30

 Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu	Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu		
			100					105						110			
Leu	Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val		
		115					120					125					
Glu	Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp		
	130					135					140						
Ile	Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn		
145					150					155					160		
Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro		
				165					170					175			
Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr		
			180					185					190				
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro		
	195					200						205					
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu		
	210					215					220						
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe		
225					230					235					240		
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His		
				245					250					255			
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser		
			260					265					270				
Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala		
	275					280						285					
Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln		
	290					295					300						
Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro		
305					310					315					320		
Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro		
			325						330					335			
Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile		
			340					345					350				
Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His		
	355					360						365					
Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr		
	370					375					380						
Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	L u	Ile	Lys	Cys		
385					390					395					400		

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
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Asp Thr Lys Asp Asp Asp Asp Lys
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<223> Description of Artificial Sequence: primer

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